

SEQUENCE LISTING

<110> Thompson, Penny J. Sheppard, Paul O. <120> Uses of Human Zven Antagonists <130> 02-22 <140> 10/680,755 <141> 2003-10-07 <150> 60/416,719 <151> 2002-10-07 <150> 60/416,718 <151> 2002-10-07 <150> 60/434,116 <151> 2002-12-16 <150> 60/433,918 <151> 2002-12-16 <150> 60/508,614 <151> 2003-10-03 <150> 60/508,603 <151> 2003-10-03 <160> 29 <170> FastSEO for Windows Version 4.0 <210> 1 <211> 1496 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (66)...(389) <400> 1 cgcccttact cactataggg ctcgagcggc cgcccgggca ggtgccgccc agtcccgagg 60 gegee atg agg age etg tge tge gee eea ete etg ete ete ttg etg etg 110 Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Leu 1 ccg ccg ctg ctc acg ccc cgc gct ggg gac gcc gcc gtg atc acc 158 Pro Pro Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr 20 25 30

ggg gct tgt gac aag gac tcc caa tgt ggt gga ggc atg tgc tgt gct

206

Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala 35 40 45	
gtc agt atc tgg gtc aag agc ata agg att tgc aca cct atg ggc aaa Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys 50 55 60	254
ctg gga gac agc tgc cat cca ctg act cgt aaa gtt cca ttt ttt ggg Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly 65 70 75	302
cgg agg atg cat cac act tgc cca tgt ctg cca ggc ttg gcc tgt tta Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu 80 85 90 95	350
cgg act tca ttt aac cga ttt att tgt tta gcc caa aag taatcgctct Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys 100 105	399
ggagtagaaa ccaaatgtga atagccacat cttacctgta aagtcttact tgtgattgtg ccaaacaaaa aatgtgccag aaagaaatgc tcttgctcc tcaactttcc aagtaacatt ttatctttg atttgtaaat gatttttt ttttttta tcgaaagaga attttactt tggatagaaa tatgaagtgt aaggcattat ggaactggt cttattccc tgtttgtt ttggtttgat ttggtttgt tcttaaatgt caaaaacgta cccattttcc caaaatagag gaaaataaga atttgatatt ttgttagaaa aacttttttt tttttttctc accaccccaa gccccatttg tgccctgccg cacaaataca cctacagctt ttggtccctt gcctctcca cctcaaagaa tttcaaggct cttaccttac	459 519 579 639 759 819 879 939 1059 1119 1239 1239 1419 1479 1496
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1 5 10 15 Pro Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr Gly 20 25 30	
Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Met Cys Cys Ala Val 35 40 45	
Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu 50 55 60	
Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg 65 70 75 80	
Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg, 85 90 95	

Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
100 105

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Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg
         75
                             80
ttc ccg gac ggc agg tac cgc tgc tcc atg gac ttg aag aac atc aat
                                                                      402
Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn
     90
                         95
ttt taggcgcttg cctggtctca ggatacccac catccttttc ctgagcacag
                                                                      455
105
cctggatttt tatttctgcc atgaaaccca gctcccatga ctctcccagt ccctacactg
                                                                      515
actaccctga tctctcttgt ctagtacgca catatgcaca caggcagaca tacctcccat
                                                                      575
catgacatgg tccccaggct ggcctgagga tgtcacagct tgaggctgtg gtgtgaaagg
                                                                      635
tggccagcct ggttctcttc cctgctcagg ctgccagaga ggtggtaaat ggcagaaagg
                                                                      695
acattecece tececteece aggtgacetg etetettee tgggeeetge eceteteece
                                                                      755
acatgtatcc ctcggtctga attagacatt cctgggcaca ggctcttggg tgcattgctc
                                                                      815
agagtcccag gtcctggcct gaccctcagg cccttcacgt gaggtctgtg aggaccaatt
                                                                      875
tgtgggtagt tcatcttccc tcgattggtt aactccttag tttcagacca cagactcaag
                                                                      935
attggctctt cccagagggc agcagacagt caccccaagg caggtgtagg gagcccaggg
                                                                      995
aggccaatca gcccctgaa gactctggtc ccagtcagcc tgtggcttgt ggcctgtgac
                                                                     1055
ctgtgacctt ctgccagaat tgtcatgcct ctgaggcccc ctcttaccac actttaccag
                                                                     1115
ttaaccactg aagccccaa ttcccacagc ttttccatta aaatgcaaat ggtggtggtt
                                                                     1175
caatctaatc tgatattgac atattagaag gcaattaggg tgtttcctta aacaactcct
                                                                     12.35
ttccaaggat cagccctgag agcaggttgg tgactttgag gagggcagtc ctctgtccag
                                                                     1295
attggggtgg gagcaaggga cagggagcag ggcaggggct gaaaggggca ctgattcaga
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                                                                     1409
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Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys
            20
                                25
Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
                            40
Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
                        55
His Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
                    70
                                        75
Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys
                85
Ser Met Asp Leu Lys Asn Ile Asn Phe
            100
                                105
<210> 6
<211> 315
<212> DNA
<213> Artificial Sequence
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<223> This degenerate sequence encodes the amino acid

60

120

180

240

300

315

sequence of SEQ ID NO:5.

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wsnythtggy thmgnggnyt nmgnatgtgy acncenythg gnmgngargg ngargartgy
cayconggnw snoayaargt noonttytty mgnaarmgna arcaycayac ntgycontgy
ytnccnaayy tnytntgyws nmgnttyccn gayggnmgnt aymgntgyws natggayytn
aaraayatha aytty
<210> 7
<211> 16
<212> PRT
<213> Arificial Sequence
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<223> Peptide linker.
<400> 7
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                                    10
<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence
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<223> Motif.
<221> VARIANT
<222> (8)...(8)
<223> Xaa is Asp or Glu.
<221> VARIANT
<222> (9)...(9)
<223> Xaa is Lys or Arg.
<221> VARIANT
<222> (1)...(10)
<223> Xaa = Any Amino Acid
<221> VARIANT
<222> (1)...(10)
<223> Xaa = Any Amino Acid
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Ala Val Ile Thr Gly Ala Cys Xaa Xaa Asp
                 5
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<210> 9

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<211> 23
<212> PRT
<213> Artificial Sequence
<220>
<223> Motif.
<221> VARIANT
<222> (4)...(4)
<223> Xaa is Gly or Leu.
<221> VARIANT
<222> (5)...(5)
<223> Xaa is Ser or Thr.
<221> VARIANT
<222> (6)...(6)
<223> Xaa is His or Arg.
<221> VARIANT
<222> (12)...(12)
<223> Xaa is any amino acid.
<221> VARIANT
<222> (13)...(13)
<223> Xaa is Lys or Arg.
<221> VARIANT
<222> (15)...(15)
<223> Xaa is any amino acid.
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                5
His Thr Cys Pro Cys Leu Pro
            20
<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Glu-Glu tag
<400> 10
Glu Tyr Met Pro Met Glu
<210> 11
<211> 249
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agetgecate caetgacteg taaagtteca ttttttggge ggaggatgea teacaettge 180
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<210> 12
<211> 68
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<213> Artificial Sequence
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<223> oligonucleotide primer ZC40821
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<223> oligonucleotide primer ZC40813
<400> 13
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<210> 14
<211> 249
<212> DNA
<213> Artificial Sequence
<220>
<223> Codon optimized polynucleotide sequence for Zven1
<400> 14
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tettgecate egetgacteg taaagtteeg ttetteggte gtegtatgea teacacetgt 180
ccgtgcctgc cgggtctggc ttgcctgcgt acctctttca accgtttcat ttgcctggct 240
cagaagtaa
<210> 15
<211> 79
<212> DNA
<213> Artificial Sequence
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<223> Oligonucleotide primer ZC45,048
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aacccaaata gaaacagca	79
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<211> 1182
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<213> Homo sapiens
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gactatgata tgcctttgga tgaagatgag gatgtgacca attccaggac gttctttgct 180
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ategecaace tggccatete tgactteetg gtggccattg tetgetgece etttgagatg 360
gactactatg tggtgcgcca gctctcctgg gagcacggcc acgtcctgtg cacctctgtc 420
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tecattetea ttgecatece ateggettae tttgeaacag aaacggteet etttattgte 600
aagagccagg agaagatctt ctgtggccag atctggcctg tggatcagca gctctactac 660
aagteetact teetetteat etttggtgte gagttegtgg geeetgtggt caccatgace 720
ctgtgctatg ccaggatctc ccgggagctc tggttcaagg cagtccctgg gttccagacg 780
gagcagattc gcaagcggct gcgctgccgc aggaagacgg tcctggtgct catgtgcatt 840
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atgaagtact tcaagaagat gatgctgctg cactggcgtc cctcccagcg ggggagcaag 1080
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ggtggaggca tgtgctgtgc tgtcagtatc tgggtcaaga gcataaggat ttgcacacct 180
atgggcaaac tgggagacag ctgccatcca ctgactcgta aagttccatt ttttgggcgg 240
aggatgcatc acacttgccc gtgtctgcca ggcttggcct gtttacggac ttcatttaac 300
cgatttattt gtttagccca aaagggtcta gaatacatgc cgatggac
<210> 26
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<223> Expression sequence with Gly linker and
     Glu-Glu-tag
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Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val
                           40
Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu
                        55
Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg
                   70
                                        75
Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg
               85
                                   90
Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys Gly Leu Glu Tyr
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Met Pro Met Asp
       115
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<211> 393
<212> PRT
<213> Homo sapiens
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Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala Thr Ser
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Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
                            40
Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
                        55
Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn
                                        75
Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
                                    90
               85
Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
                               105
Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
       115
                            120
                                                125
Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
                        135
                                           140
Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
                   150
                                        155
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
               165
                                    170
Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu
           180
                               185
Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
                            200
                                                205
Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
                        215
                                            220
Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
                   230
                                       235
Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
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250

245

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Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
          260
                               265
Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
                           280
                                               285
Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
                       295
Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
                   310
                                        315
Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
               325
                                    330
Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
                                345
Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
       355
                           360
                                               365
Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
                       375
Glu Glu Val Asp Cys Ile Arg Leu Lys
                   390
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<210> 28 <211> 384

<212> PRT

<213> Homo sapiens

<400> 28

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Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys 260 265 Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp 280 Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val 295 300 Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys 310 315 Ile Ala Met Ser Asn Ser Met Ile Asn Thr Val Cys Phe Val Thr Val 330 325 Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met Met Leu Leu His Trp 340 345 Arg Pro Ser Gln Arg Gly Ser Lys Ser Ser Ala Asp Leu Asp Leu Arg 360 365 Thr Asn Gly Val Pro Thr Thr Glu Glu Val Asp Cys Ile Arg Leu Lys 375 380

<210> 29

<211> 129

<212> PRT

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Lys